In the Official Action mailed September 28, 1999 the pending claims were rejected under 35 U.S.C. § 112, second paragraph, for failing to particularly point out and distinctly claim the subject matter of the present invention. Specifically, the Office contended that the recitation of "maximal amino acid alignment" is indefinite because the claimed polypeptide sequences can be aligned in different ways with the reference sequence due to the presence of gaps, and it is not clear which alignment is the maximal alignment in the absence of a scoring rule with specified parameters. The applicants respectfully disagree.

The specification teaches at page 7, lines 25-32, page 11, lines 5-13, and Figures 1-3, 8, and 9 that maximal alignment is achieved by employing the following algorithm: align the sequences, including by inserting vacant positions, so that the *maximal number of identical amino acids are found*. Thus, the applicants do not merely disclose the desired result of maximal alignment as alleged in the Office Action, but teach the parameters used to achieve it. The art recognizes this as a valid method of sequence alignment, as evidenced by the teachings of George et al., which describes different types of scoring rules, including those that assign a score to *identically matched residues only* (D. Schlesinger, Ed., Macromolecular Sequencing and Synthesis, Ch. 12 (Alan R. Liss, Inc. New York, 1988) at page 132, column 1, paragraph 2). Further, it is customary to insert vacant positions or "gaps" in sequence alignments to maintain the proper association between residues, as explained in George et al. at page 128, column 1, paragraph 3.

Consequently, one skilled in the art would understand the metes and bounds of the claims because he would understand that the sequence alignment to which the claims refer is an art recognized one in which maximal alignment is achieved by matching the number of identical amino acids using insertion of vacant positions.

<u>The Pending § 102(b) Rejections</u>

Legrain et al., Gene, 130:73-80 (1993); Quentin-Millet WO 93/06861

In addition, the pending claims were rejected under 35 U.S.C. § 102(b) as being unpatentable over either Legrain et al. or Quentin-Millet. The Office has alleged that because the present claims use comprising language and since the metes and bounds of the term "maximal amino acid alignment" is allegedly not clear, the IM2169 and IM2394 Tbp2 subunits provided in Legrain et al. or Quentin-Millet anticipate the present claims.

A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described. *Verdegaal Bros. v. Union Oil Co. of California, 814 F.2d 628 (Fed. Cir. 1987)*; M.P.E.P. § 2131. Thus, the cited prior art must teach or suggest an IM2169- or an IM2394-type Tbp2 protein having at least one of its domains totally or partially deleted. However, the Legrain et al. and Quentin-Millet references only provide the full-length amino acid sequence of the IM2169 and IM2394 reference Tbp2 proteins. While the Examiner correctly points out that the amino acid sequences disclosed in both references are identical to SEQ ID NO: 2 and SEQ ID NO: 4, the claims do not encompass SEQ ID NO: 2 or SEQ ID NO: 4. Accordingly, the applicants submit that neither Legrain et al. nor Quentin-Millet anticipate the present claims.
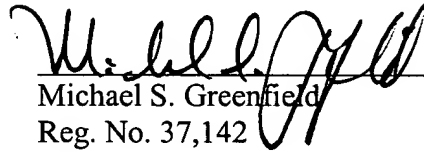
<u>Conclusion</u>

Entry of the foregoing amendments and early and favorable consideration of the subject application is respectfully requested. If, in the opinion of the Examiner, a telephone conference

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would expedite the prosecution of this application, the Examiner is invited to call the undersigned attorney.

Respectfully submitted,

McDONNELL BOEHNEN
HULBERT & BERGHOFF

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Michael S. Greenfield
Reg. No. 37,142

McDONNELL BOEHNEN
HULBERT & BERGHOFF
300 South Wacker Drive, Suite 3200
Chicago, Illinois 60606
312-913-0001; Facsimile: 312-913-0002